



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.

(ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
CELL LOCUS-1

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-034

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864/9741
(C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
 20 25 30
 Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
 35 40 45
 Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
 50 55 60
 Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
 65 70 75 80
 Leu Pro Leu Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
 20 25 30
 Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 35 40 45
 Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
 50 55 60
 Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
 65 70 75 80
 Leu Pro Val Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
 20 25 30
 His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
 35 40 45
 Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
 50 55 60
 Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
 65 70 75 80
 Ile Pro Lys Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
 20 25 30
 Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
 35 40 45
 Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
 50 55 60
 Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1 5 10 15
Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
20 25 30
Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45
Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
50 55 60
Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65 70 75 80
Arg Pro Val Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1 5 10 15
Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
20 25 30
Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
35 40 45
Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60
Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65 70 75 80
Ile Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1 5 10 15
Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
20 25 30
Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
35 40 45
Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
50 55 60
Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65 70 75 80
His Pro Leu Thr Xaa
85

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Leu Xaa Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15
Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
20 25 30
Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
50 55 60
Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65 70 75 80
Xaa Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|--|------|
| GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA | 60 |
| TTCCCAGTGG CCTTGATATT TAACTGATT CCTGCCACCA GGTCCTTGGG CCACCCTGTC | 120 |
| CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCGCTCC TGGCCTCAGG | 180 |
| CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCG | 240 |
| CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGGGTGCGCG CACGGAAATC | 300 |
| GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC | 360 |
| AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG | 420 |
| TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTC | 480 |
| AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG | 540 |
| TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCC GGACCA GCCCAGGTCA | 600 |
| CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT | 651 |
| Met Lys His Leu Val Ala Ala Trp Leu Leu Val | |
| 1 5 10 | |
| GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC | 699 |
| Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn | |
| 15 20 25 | |
| CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT | 747 |
| Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp | |
| 30 35 40 | |
| GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC | 795 |
| Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys | |
| 45 50 55 | |
| TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA | 843 |
| Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala | |
| 60 65 70 75 | |
| GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA | 891 |
| Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile | |
| 80 85 90 | |
| AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT | 939 |
| Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys | |
| 95 100 105 | |
| CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT | 987 |
| Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys | |
| 110 115 120 | |
| GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT | 1035 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Glu | Ala | Glu | Pro | Cys | Arg | Asn | Gly | Gly | Ile | Cys | Thr | Asp | Leu | Val | Ala | | |
| 125 | | | | | | 130 | | | | 135 | | | | | | | |
| AAC | TAC | TCT | TGT | GAA | TGC | CCA | GGA | GAA | TTT | ATG | GGA | CGA | AAT | TGT | CAA | 1083 | |
| Asn | Tyr | Ser | Cys | Glu | Cys | Pro | Gly | Glu | Phe | Met | Gly | Arg | Asn | Cys | Gln | | |
| 140 | | | | | 145 | | | | | 150 | | | | | 155 | | |
| TAT | AAA | TGC | TCT | GGG | CAC | TTG | GGA | ATC | GAA | GGT | GGG | ATC | ATA | TCT | AAT | 1131 | |
| Tyr | Lys | Cys | Ser | Gly | His | Leu | Gly | Ile | Glu | Gly | Gly | Ile | Ile | Ser | Asn | | |
| | | | | 160 | | | | | 165 | | | | | 170 | | | |
| CAG | CAA | ATC | ACA | GCT | TCA | TCT | AAT | CAC | CGA | GCT | CTT | TTT | GGA | CTC | CAG | 1179 | |
| Gln | Gln | Ile | Thr | Ala | Ser | Ser | Asn | His | Arg | Ala | Leu | Phe | Gly | Leu | Gln | | |
| | | | 175 | | | | | 180 | | | | | 185 | | | | |
| AAG | TGG | TAT | CCC | TAC | TAT | GCT | CGA | CTT | AAT | AAG | AAG | GGC | CTT | ATA | AAT | 1227 | |
| Lys | Trp | Tyr | Pro | Tyr | Tyr | Ala | Arg | Leu | Asn | Lys | Lys | Gly | Leu | Ile | Asn | | |
| | | 190 | | | | | 195 | | | | | 200 | | | | | |
| GCC | TGG | ACA | GCT | GCT | GAA | AAT | GAC | AGA | TGG | CCA | TGG | ATT | CAG | ATA | AAT | 1275 | |
| Ala | Trp | Thr | Ala | Ala | Glu | Asn | Asp | Arg | Trp | Pro | Trp | Ile | Gln | Ile | Asn | | |
| | 205 | | | | | 210 | | | | | 215 | | | | | | |
| TTG | CAA | AGA | AAA | ATG | AGA | GTC | ACT | GGT | GTT | ATT | ACC | CAA | GGA | GCA | AAA | 1323 | |
| Leu | Gln | Arg | Lys | Met | Arg | Val | Thr | Gly | Val | Ile | Thr | Gln | Gly | Ala | Lys | | |
| 220 | | | | | 225 | | | | | 230 | | | | | 235 | | |
| AGG | ATT | GGA | AGC | CCA | GAG | TAC | ATA | AAA | TCC | TAC | AAA | ATT | GCC | TAC | AGC | 1371 | |
| Arg | Ile | Gly | Ser | Pro | Glu | Tyr | Ile | Lys | Ser | Tyr | Lys | Ile | Ala | Tyr | Ser | | |
| | | | | 240 | | | | | 245 | | | | | 250 | | | |
| AAT | GAC | GGG | AAG | ACC | TGG | GCA | ATG | TAC | AAA | GTA | AAA | GGC | ACC | AAT | GAA | 1419 | |
| Asn | Asp | Gly | Lys | Thr | Trp | Ala | Met | Tyr | Lys | Val | Lys | Gly | Thr | Asn | Glu | | |
| | | | 255 | | | | | 260 | | | | | 265 | | | | |
| GAG | ATG | GTC | TTT | CGT | GGA | AAT | GTT | GAT | AAC | AAC | ACA | CCA | TAT | GCT | AAT | 1467 | |
| Glu | Met | Val | Phe | Arg | Gly | Asn | Val | Asp | Asn | Asn | Thr | Pro | Tyr | Ala | Asn | | |
| | | 270 | | | | | 275 | | | | | 280 | | | | | |
| TCT | TTC | ACA | CCC | CCA | ATC | AAA | GCT | CAG | TAT | GTA | AGA | CTC | TAC | CCC | CAA | 1515 | |
| Ser | Phe | Thr | Pro | Pro | Ile | Lys | Ala | Gln | Tyr | Val | Arg | Leu | Tyr | Pro | Gln | | |
| | 285 | | | | | 290 | | | | | 295 | | | | | | |
| ATT | TGT | CGA | AGG | CAT | TGT | ACT | TTA | AGA | ATG | GAA | CTT | CTT | GGC | TGT | GAG | 1563 | |
| Ile | Cys | Arg | Arg | His | Cys | Thr | Leu | Arg | Met | Glu | Leu | Leu | Gly | Cys | Glu | | |
| 300 | | | | | 305 | | | | | 310 | | | | | 315 | | |
| CTC | TCA | GGC | TGT | TCA | GAA | CCT | TTG | GGG | ATG | AAA | TCA | GGG | CAT | ATA | CAA | 1611 | |
| Leu | Ser | Gly | Cys | Ser | Glu | Pro | Leu | Gly | Met | Lys | Ser | Gly | His | Ile | Gln | | |
| | | | | 320 | | | | | 325 | | | | | 330 | | | |
| GAC | TAC | CAG | ATC | ACT | GCC | TCC | AGC | GTC | TTC | AGA | ACA | CTC | AAC | ATG | GAC | 1659 | |
| Asp | Tyr | Gln | Ile | Thr | Ala | Ser | Ser | Val | Phe | Arg | Thr | Leu | Asn | Met | Asp | | |
| | | | 335 | | | | | 340 | | | | | 345 | | | | |
| ATG | TTT | ACT | TGG | GAA | CCA | AGG | AAA | GCC | AGG | CTG | GAC | AAG | CAA | GGC | AAA | 1707 | |
| Met | Phe | Thr | Trp | Glu | Pro | Arg | Lys | Ala | Arg | Leu | Asp | Lys | Gln | Gly | Lys | | |
| | | 350 | | | | | 355 | | | | | 360 | | | | | |
| GTA | AAT | GCC | TGG | ACT | TCC | GGC | CAT | AAC | GAC | CAG | TCA | CAA | TGG | TTA | CAG | 1755 | |
| Val | Asn | Ala | Trp | Thr | Ser | Gly | His | Asn | Asp | Gln | Ser | Gln | Trp | Leu | Gln | | |
| | 365 | | | | | 370 | | | | | 375 | | | | | | |

| | |
|---|------|
| GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly 380 385 390 395 | 1803 |
| GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala 400 405 410 | 1851 |
| TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln 415 420 425 | 1899 |
| AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg 430 435 440 | 1947 |
| AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu 445 450 455 | 1995 |
| CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly 460 465 470 475 | 2043 |
| TGC GCA GAG GAG GAA TGAAGTGC GGCCGCACAT CCCACAATGC TTTTCTTTAT Cys Ala Glu Glu Glu 480 | 2098 |
| TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAAACT GCATTTGTTT | 2158 |
| TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG | 2218 |
| CCTTTTAAAT AATTTAATTT GGTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT | 2278 |
| CTGTGAGTTA CTCTTCTTGT TCTCT | 2303 |

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| |
|--|
| Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly 1 5 10 15 |
| Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu 20 25 30 |
| Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys 35 40 45 |
| Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu 50 55 60 |
| Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro 65 70 75 80 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Pro | Cys | His | Asn | Gly | Gly | Thr | Cys | Glu | Ile | Ser | Glu | Ala | Tyr | Arg | |
| | | | | 85 | | | | | 90 | 1 | | | | 95 | | |
| Gly | Asp | Thr | Phe | Ile | Gly | Tyr | Val | Cys | Lys | Cys | Pro | Arg | Gly | Phe | Asn | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gly | Ile | His | Cys | Gln | His | Asn | Ile | Asn | Glu | Cys | Glu | Ala | Glu | Pro | Cys | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Arg | Asn | Gly | Gly | Ile | Cys | Thr | Asp | Leu | Val | Ala | Asn | Tyr | Ser | Cys | Glu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Cys | Pro | Gly | Glu | Phe | Met | Gly | Arg | Asn | Cys | Gln | Tyr | Lys | Cys | Ser | Gly | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| His | Leu | Gly | Ile | Glu | Gly | Gly | Ile | Ile | Ser | Asn | Gln | Gln | Ile | Thr | Ala | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Ser | Ser | Asn | His | Arg | Ala | Leu | Phe | Gly | Leu | Gln | Lys | Trp | Tyr | Pro | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Tyr | Ala | Arg | Leu | Asn | Lys | Lys | Gly | Leu | Ile | Asn | Ala | Trp | Thr | Ala | Ala | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Glu | Asn | Asp | Arg | Trp | Pro | Trp | Ile | Gln | Ile | Asn | Leu | Gln | Arg | Lys | Met | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Arg | Val | Thr | Gly | Val | Ile | Thr | Gln | Gly | Ala | Lys | Arg | Ile | Gly | Ser | Pro | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Glu | Tyr | Ile | Lys | Ser | Tyr | Lys | Ile | Ala | Tyr | Ser | Asn | Asp | Gly | Lys | Thr | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Trp | Ala | Met | Tyr | Lys | Val | Lys | Gly | Thr | Asn | Glu | Glu | Met | Val | Phe | Arg | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Gly | Asn | Val | Asp | Asn | Asn | Thr | Pro | Tyr | Ala | Asn | Ser | Phe | Thr | Pro | Pro | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ile | Lys | Ala | Gln | Tyr | Val | Arg | Leu | Tyr | Pro | Gln | Ile | Cys | Arg | Arg | His | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Cys | Thr | Leu | Arg | Met | Glu | Leu | Leu | Gly | Cys | Glu | Leu | Ser | Gly | Cys | Ser | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Glu | Pro | Leu | Gly | Met | Lys | Ser | Gly | His | Ile | Gln | Asp | Tyr | Gln | Ile | Thr | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Ala | Ser | Ser | Val | Phe | Arg | Thr | Leu | Asn | Met | Asp | Met | Phe | Thr | Trp | Glu | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Pro | Arg | Lys | Ala | Arg | Leu | Asp | Lys | Gln | Gly | Lys | Val | Asn | Ala | Trp | Thr | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Ser | Gly | His | Asn | Asp | Gln | Ser | Gln | Trp | Leu | Gln | Val | Asp | Leu | Leu | Val | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Pro | Thr | Lys | Val | Thr | Gly | Ile | Ile | Thr | Gln | Gly | Ala | Lys | Asp | Phe | Gly | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| His | Val | Gln | Phe | Val | Gly | Ser | Tyr | Lys | Leu | Ala | Tyr | Ser | Asn | Asp | Gly | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430
Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445
Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460
Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys 1 5 10 15 | 48 |
| CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT Arg * Gly Lys Arg Thr Ser Ser * Ile Leu * * Gly Arg Ser 20 25 30 | 96 |
| CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr 35 40 45 | 144 |
| ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg 50 55 60 | 192 |
| TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln 65 70 75 80 | 240 |
| TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly 85 90 95 | 288 |
| ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro 100 105 110 | 336 |
| GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser 115 120 125 | 384 |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GAT Asp 130 | GAA Glu 130 | GAA Glu 130 | GAA Glu 130 | CCA Pro 130 | ACT Thr 130 | TCA Ser 135 | GCA Ala 135 | GGT Gly 135 | CCC Pro 135 | TGC Cys 140 | ACT Thr 140 | CCT Pro 140 | AAT Asn 140 | CCA Pro 140 | TGC Cys 140 | 432 |
| CAT His 145 | AAT Asn 145 | GGA Gly 145 | GGA Gly 145 | ACC Thr 145 | TGT Cys 150 | GAA Glu 150 | ATA Ile 150 | AGT Ser 150 | GAA Glu 155 | GCA Ala 155 | TAC Tyr 155 | CGA Arg 155 | GGG Gly 155 | GAT Asp 160 | ACA Thr 160 | 480 |
| TTC Phe 165 | ATA Ile 165 | GGC Gly 165 | TAT Tyr 165 | GTT Val 165 | TGT Cys 165 | AAA Lys 165 | TGT Cys 165 | CCC Pro 170 | CGA Arg 170 | GGA Gly 170 | TTT Phe 170 | AAT Asn 170 | GGG Gly 175 | ATT Ile 175 | CAC His 175 | 528 |
| TGT Cys 180 | CAG Gln 180 | CAC His 180 | AAC Asn 180 | ATA Ile 180 | AAT Asn 180 | GAA Glu 185 | TGC Cys 185 | GAA Glu 185 | GTT Val 185 | GAG Glu 185 | CCT Pro 190 | TGC Cys 190 | AAA Lys 190 | AAT Asn 190 | GGT Gly 190 | 576 |
| GGA Gly 195 | ATA Ile 195 | TGT Cys 195 | ACA Thr 195 | GAT Asp 195 | CTT Leu 195 | GTT Val 200 | GCT Ala 200 | AAC Asn 200 | TAT Tyr 200 | TCC Ser 205 | TGT Cys 205 | GAG Glu 205 | TGC Cys 205 | CCA Pro 205 | GGC Gly 205 | 624 |
| GAA Glu 210 | TTT Phe 210 | ATG Met 210 | GGA Gly 210 | AGA Arg 210 | AAT Asn 215 | TGT Cys 215 | CAA Gln 215 | TAC Tyr 215 | AAA Lys 215 | TGC Cys 220 | TCA Ser 220 | GGC Gly 220 | CCA Pro 220 | CTG Leu 220 | GGA Gly 220 | 572 |
| ATT Ile 225 | GAA Glu 225 | GGT Gly 225 | GGA Gly 225 | ATT Ile 230 | ATA Ile 230 | TCA Ser 230 | AAC Asn 230 | CAG Gln 235 | CAA Gln 235 | ATC Ile 235 | ACA Thr 235 | GCT Ala 235 | TCC Ser 235 | TCT Ser 240 | ACT Thr 240 | 720 |
| CAC His 245 | CGA Arg 245 | GCT Ala 245 | CTT Leu 245 | TTT Phe 245 | GGA Gly 245 | CTC Leu 245 | CAA Gln 250 | AAA Lys 250 | TGG Trp 250 | TAT Tyr 250 | CCC Pro 250 | TAC Tyr 250 | TAT Tyr 255 | GCA Ala 255 | CGT Arg 255 | 768 |
| CTT Leu 260 | AAT Asn 260 | AAG Lys 260 | AAG Lys 260 | GGG Gly 260 | CTT Leu 260 | ATA Ile 265 | AAT Asn 265 | GCG Ala 265 | TGG Trp 265 | ACA Thr 265 | GCT Ala 270 | GCA Ala 270 | GAA Glu 270 | AAT Asn 270 | GAC Asp 270 | 816 |
| AGA Arg 275 | TGG Trp 275 | AAG Lys 275 | CGG Arg 275 | TGG Trp 275 | ATT Ile 280 | CAG Gln 280 | ATA Ile 280 | AAT Asn 280 | TTG Leu 280 | CAA Gln 285 | AGA Arg 285 | AAA Lys 285 | ATG Met 285 | AGA Arg 285 | GTT Val 285 | 864 |
| ACT Thr 290 | GGT Gly 290 | GTG Val 290 | ATT Ile 290 | ACC Thr 290 | CAA Gln 295 | GGG Gly 295 | GCC Ala 295 | AAG Lys 295 | AGG Arg 295 | ATT Ile 300 | GGA Gly 300 | AGC Ser 300 | CCA Pro 300 | GAG Glu 300 | TAT Tyr 300 | 912 |
| ATA Ile 305 | AAA Lys 305 | TTC Phe 305 | TAC Tyr 305 | AAA Lys 310 | ATT Ile 310 | GCC Ala 310 | TAC Tyr 310 | AGT Ser 315 | AAT Asn 315 | GAT Asp 315 | GGA Gly 315 | AAG Lys 315 | ACT Thr 315 | TGG Trp 320 | GCA Ala 320 | 960 |
| ATG Met 325 | TAC Tyr 325 | AAA Lys 325 | GTG Val 325 | AAA Lys 325 | GGC Gly 325 | ACC Thr 330 | AAT Asn 330 | GAA Glu 330 | GAC Asp 330 | ATG Met 330 | GTG Val 335 | TTT Phe 335 | CGT Arg 335 | GGA Gly 335 | AAC Asn 335 | 1008 |
| ATT Ile 340 | GAT Asp 340 | AAC Asn 340 | AAC Asn 340 | ACT Thr 340 | CCA Pro 345 | TAT Tyr 345 | GCT Ala 345 | AAC Asn 345 | TCT Ser 345 | TTC Phe 345 | ACA Thr 350 | CCC Pro 350 | CCC Pro 350 | ATA Ile 350 | AAA Lys 350 | 1056 |
| GCT Ala 355 | CAG Gln 355 | TAT Tyr 355 | GTA Val 355 | AGA Arg 355 | CTC Leu 355 | TAT Tyr 360 | CCC Pro 360 | CAA Gln 360 | GTT Val 360 | TGT Cys 365 | CGA Arg 365 | AGA Arg 365 | CAT His 365 | TGC Cys 365 | ACT Thr 365 | 1104 |
| TTG Leu 370 | CGA Arg 370 | ATG Met 370 | GAA Glu 370 | CTT Leu 375 | CTT Leu 375 | GGC Gly 375 | TGT Cys 375 | GAA Glu 380 | CTG Leu 380 | TCG Ser 380 | GGT Gly 380 | TGT Cys 380 | TCT Ser 380 | GAG Glu 380 | CCT Pro 380 | 1152 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CTG | GGT | ATG | AAA | TCA | GGA | CAT | ATA | CAA | GAC | TAT | CAG | ATC | ACT | GCC | TCC | 1200 |
| Leu | Gly | Met | Lys | Ser | Gly | His | Ile | Gln | Asp | Tyr | Gln | Ile | Thr | Ala | Ser | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| AGC | ATC | TTC | AGA | ACG | CTC | AAC | ATG | GAC | ATG | TTC | ACT | TGG | GAA | CCA | AGG | 1248 |
| Ser | Ile | Phe | Arg | Thr | Leu | Asn | Met | Asp | Met | Phe | Thr | Trp | Glu | Pro | Arg | |
| | | | | 405 | | | | | 410 | | | | | | 415 | |
| AAA | GCT | CGG | CTG | GAC | AAG | CAA | GGC | AAA | GTG | AAT | GCC | TGG | ACC | TCT | GGC | 1296 |
| Lys | Ala | Arg | Leu | Asp | Lys | Gln | Gly | Lys | Val | Asn | Ala | Trp | Thr | Ser | Gly | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| CAC | AAT | GAC | CAG | TCA | CAA | TGG | TTA | CAG | GTG | GAT | CTT | CTT | GTT | CCA | ACC | 1344 |
| His | Asn | Asp | Gln | Ser | Gln | Trp | Leu | Gln | Val | Asp | Leu | Leu | Val | Pro | Thr | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| AAA | GTG | ACT | GGC | ATC | ATT | ACA | CAA | GGA | GCT | AAA | GAT | TTT | GGT | CAT | GTA | 1392 |
| Lys | Val | Thr | Gly | Ile | Ile | Thr | Gln | Gly | Ala | Lys | Asp | Phe | Gly | His | Val | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| CAG | TTT | GTT | GGC | TCC | TAC | AAA | CTG | GCT | TAC | AGC | AAT | GAT | GGA | GAA | CAC | 1440 |
| Gln | Phe | Val | Gly | Ser | Tyr | Lys | Leu | Ala | Tyr | Ser | Asn | Asp | Gly | Glu | His | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| TGG | ACT | GTA | TAC | CAG | GAT | GAA | AAG | CAA | AGA | AAA | GAT | AAG | GTT | TTC | CAG | 1488 |
| Trp | Thr | Val | Tyr | Gln | Asp | Glu | Lys | Gln | Arg | Lys | Asp | Lys | Val | Phe | Gln | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| GGA | AAT | TTT | GAC | AAT | GAC | ACT | CAC | AGA | AAA | AAT | GTC | ATC | GAC | CCT | CCC | 1536 |
| Gly | Asn | Phe | Asp | Asn | Asp | Thr | His | Arg | Lys | Asn | Val | Ile | Asp | Pro | Pro | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| ATC | TAT | GCA | CGA | CAC | ATA | AGA | ATC | CTT | CCT | TGG | TCC | TGG | TAC | GGG | AGG | 1584 |
| Ile | Tyr | Ala | Arg | His | Ile | Arg | Ile | Leu | Pro | Trp | Ser | Trp | Tyr | Gly | Arg | |
| | | 515 | | | | | 520 | | | | | 525 | | | | |
| ATC | ACA | TTG | GCG | TCA | GAG | CTG | CTG | GGC | TGC | ACA | GAG | GAG | GAA | TGA | GGG | 1632 |
| Ile | Thr | Leu | Ala | Ser | Glu | Leu | Leu | Gly | Cys | Thr | Glu | Glu | Glu | * | Gly | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| GAG | GCT | ACA | TTT | CAC | AAC | CGT | CTT | CCC | TAT | TTG | GGT | AAA | AGT | ATC | TCC | 1680 |
| Glu | Ala | Thr | Phe | His | Asn | Arg | Leu | Pro | Tyr | Leu | Gly | Lys | Ser | Ile | Ser | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| ATG | GAA | TGA | ACT | GTG | TAA | AAT | CTG | TAG | GAA | ACT | GAA | TGG | TTT | TTT | TTT | 1728 |
| Met | Glu | * | Thr | Val | * | Asn | Leu | * | Glu | Thr | Glu | Trp | Phe | Phe | Phe | |
| | | | | 565 | | | | | 570 | | | | | 575 | | |
| TTT | TCA | TGA | AAA | AGT | GGT | CAA | ATT | ATG | GTA | GGC | AAC | TAA | CGG | TGT | TTT | 1776 |
| Phe | Ser | * | Lys | Ser | Gly | Gln | Ile | Met | Val | Gly | Asn | * | Arg | Cys | Phe | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| TAC | C | | | | | | | | | | | | | | | 1780 |
| Tyr | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Lys Arg Thr Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu * * Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser
1 5 10 15

Ala Thr Leu Pro Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro
20 25 30

Gly Asp Gly Ile Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly
35 40 45

Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro
50 55 60

Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly
65 70 75 80

Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser
85 90 95

Ser Val Val Glu Val Ala Ser Asp Glu Glu Pro Thr Ser Ala Gly
100 105 110

Pro Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser
115 120 125

Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro
130 135 140

Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu
145 150 155 160

Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn
 165 170 175
 Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr
 180 185 190
 Lys Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln
 195 200 205
 Gln Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys
 210 215 220
 Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala
 225 230 235 240
 Trp Thr Ala Ala Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn
 245 250 255
 Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
 260 265 270
 Arg Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser
 275 280 285
 Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
 290 295 300
 Asp Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn
 305 310 315 320
 Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
 325 330 335
 Val Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
 340 345 350
 Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
 355 360 365
 Asp Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp
 370 375 380
 Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
 385 390 395 400
 Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
 405 410 415
 Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
 420 425 430
 Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
 435 440 445
 Tyr Ser Asn Asp Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln
 450 455 460
 Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
 465 470 475 480
 Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu
 485 490 495

Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly
 500 505 510
 Cys Thr Glu Glu Glu
 515

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
 1 5 10 15
 Ser Met Glu * Thr Val * Asn Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Phe Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTATT | 60 |
| ACCCAAGGAG CAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC | 120 |
| AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC | 180 |
| TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA | 240 |
| GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA | 300 |
| CTTCTTGGCT GTGAGCTC | 318 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | |
|---|--|
| Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln | |
| 1 5 10 15 | |
| Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp | |
| 20 25 30 | |
| Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp | |
| 35 40 45 | |
| His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu | |
| 50 55 60 | |
| Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg | |
| 65 70 75 80 | |
| Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu | |
| 85 90 95 | |

Asp Gly Xaa Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp
 100 105 110
 Lys Glu Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met
 115 120 125
 Phe Asn Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser
 130 135 140
 Cys His Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160
 His Gly Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp
 165 170 175
 Ser Gln Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala
 180 185 190
 Phe Gly Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Lys Ile
 195 200 205
 Asn Ala Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val
 210 215 220
 Asp Leu Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240
 Arg Asp Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His
 245 250 255
 Ser Asp Asp Gly Val Gln Trp Thr Val Tyr Xaa Xaa Glu Glu Gln Gly
 260 265 270
 Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys
 275 280 285
 Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
 290 295 300
 Val Ser Trp His Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
 1 5 10 15
 Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp
 20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
 35 40 45
 Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
 50 55 60
 Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
 65 70 75 80
 Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
 85 90 95
 Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
 100 105 110
 Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
 115 120 125
 Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
 130 135 140
 Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160
 Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
 165 170 175
 Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
 180 185 190
 Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
 195 200 205
 Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
 210 215 220
 Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240
 Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
 245 250 255
 Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
 260 265 270
 Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
 275 280 285
 Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
 290 295 300
 Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
 305 310 315 320
 Thr

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1 5 10 15
Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
20 25 30
Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
35 40 45
Glu Glu Glu Pro Thr Ser Ala Gly Pro
50 55

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15
Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
 1 5 10 15
 Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
 20 25 30
 Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
 20 25 30
 Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
 35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|-----|
| NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT | 60 |
| GTAGGTTTCCT TTTCCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACCTG TTCTAGTGTT | 120 |
| GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT | 180 |
| GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT | 240 |
| GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA | 300 |
| ATATGTACAG | 310 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 549..1211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|-----|
| GAATTCCGGG AGGGAGGGTA GGGGGCGGG CCGCGGGGG CCAAAGCCAG CTAGGCTCAG | 60 |
| TCTCACACGC GCGCCGCCAC TGTTTGTATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC | 120 |
| CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC | 180 |
| GTGAGCCGTA GTCAGTCTG GCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA | 240 |
| GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC | 300 |
| CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA | 360 |
| ATCACCCCTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCAAGATTT GAGAAGCGCT | 420 |
| GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG | 480 |
| CGCGCCTCGC CTAAGTGCC CTCCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA | 540 |
| GAAGGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGACTCAG CCTCGGGGTG | 600 |
| CCCCAGTTCT GCAAAGGTGA CATTGCAAC CCGAACCCT GTGAAAATGG TGGCATCTGT | 660 |
| CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGTC CAGAAGGCTT CGCAGGTCCG | 720 |
| AACTGCTCTA GTGTTGTGGA GGTGTCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC | 780 |
| TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA | 840 |

| | |
|--|------|
| GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG | 900 |
| CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT | 960 |
| GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA | 1020 |
| TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA | 1080 |
| TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT | 1140 |
| AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTCAG | 1200 |
| GTAACAGTGG GATGAGACAA ATCCATTTCC CAAATTATCA GAATCATTAT AGAAGTAGGT | 1260 |
| TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTAAAATG TGATTTAGTT CAGAATTAAC | 1320 |
| ATGGTTGGAA ACTCTAAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA | 1380 |
| ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG | 1440 |
| AAAAAGATCT TATCATTTCA TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA | 1500 |
| TAAATACCTA ATTGAAAAAA GTTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTCAGAG | 1560 |
| ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTGTGAGA AATAGTTTCC CATGTGCAA | 1620 |
| TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA | 1680 |
| TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTACTACAGA | 1740 |
| AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA | 1800 |
| TAGCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAGCAG AAATGAGATG | 1860 |
| TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT | 1920 |
| CTTTAAGATA GTCACATAACA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG | 1980 |
| TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAAG TTTTGAAATA | 2040 |
| AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAATCAAC | 2100 |
| AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG | 2160 |
| GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG | 2220 |
| TGCCACATTT TGTTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC | 2280 |
| ACTATAATTT GAATAAAAGC CGGAATTC | 2308 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ser | Val | Ala | Val | Trp | Leu | Leu | Val | Gly | Leu | Ser | Leu | Gly |
| 1 | | | | | | | | | | | | | | | |
| | | | | 5 | | | | | 10 | | | | | 15 | |

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 355 360 365
 Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu
 370 375 380
 Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa
 385 390 395 400
 Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 405 410 415
 Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys
 420 425 430
 Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 435 440 445
 Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 450 455 460
 Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 465 470 475
 Glu
 480